SEQUENCE LISTING

\\10> National Institute of Agrobiological Sciences

<120> Sodium/Proton antiporter gene

<130> MOA-006PCT

<150> JP 1998-365604

<151> 1998-12-22

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<170> PatentIn Ver. 2.0

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<212> DNA

<213> Oryza sativa

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tctgcgaatc gaattcttig titititic tctaattita ccgggaatig tcgaattagg 180

cattcaccaa cgagcaagag gggagtggat tggttggtta aagciccgca tcttgcggcg 240

gaaatctcgc tctctictci gcggtggtg gccggagaag tcgccgccgg tgaggc atg 299

Met

ggg atg gag gtg gcg gcg cgg ctg ggg gct ctg tac acg acc tcc 347 Gly Met Glu Val Ala Ala Ala Arg Leu Gly Ala Leu Tyr Thr Thr Ser 5 10 15

gac tac gcg tcg gtg gtg tcc atc aac ctg ttc gtc gcg ctg ctc tgc 395

Asp Tyr Ala Ser Val Val Ser Ile Asn Leu Phe Val Ala Leu Leu Cys

20 25 30

gcc tgc atc gtc ctc ggc cac ctc ctc gag gag aat cgc tgg gtc aat

Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val Asn

35

40

45

gag too are acc gcg cic are are ggg cic igc acc ggc gig gig are 491 Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val Ile

ttg	ctg	a t	g a	acc	aaa	ggg	aag	agc	tcg	cac	tta	ttc	gtc	ttc	agt	gag	539
Leu	Leu	Мe	t :	Thr	Lys	Gly	Lys	Ser	Ser	His	Leu	Phe	Val	Phe	Ser	Glu	
				-	70					75					80		
gat	ctc	t t	c	ttc	atc	tac	ctc	ctc	cct	ccg	atc	atc	ttc	aat	gca	ggt	587
Asp	Leu	Pt	ıe	Phe	He	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe	Asn	Ala	Gly	
				85					90					95			
ttt	cag	g	t a	aag	aaa	aag	caa	ttc	ttc	cgg	aat	ttc	atg	acg	atc	aca	635
												Phe					
			00					105					110				
tta	1 II	t g	ga	gcc	gto	ggg	aca	atg	ata	tcc	ttt	ttc	aca	ata	tct	att	683
																·Ile	
	11						120					125					
		-															
σr	t gc	c a	ıtt	gca	a ata	a tte	c ag	c aga	a atg	g aac	c at	t gga	a acg	g cts	g ga	t gta	731
																p Val	
13				•••	_	13					14					145	
10	U																
aa	a an	t ·	+ + +	c t	t ør	a at	t gg	a gc	c at	ctt	t tc	t gc	g ac	a ga	t tc	t gtc	779
																r Val	
υl	y AS	PΙ	1116	, LC	u ni 15			,	•	15					16		
					1 9	U					~						

tor	aca	ttg	cag	gtc	ctc	aat	cag	gat	gag	aca	ссс	ttt	ttg	tac	agt	827
Cvs	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Phe	Leu	Tyr	Ser	
			165										175			

- ctg gta ttc ggt gaa ggt gtt gtg aac gat gct aca tca att gtg ctt 875 Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Ile Val Leu 180 185 190
- ttc aac gca cta cag aac ttt gat ctt gtc cac ata gat gcg gct gtc 923 Phe Asn Ala Leu Gln Asn Phe Asp Leu Val His Ile Asp Ala Ala Val 195 200 205
- gtt ctg aaa ttc ttg ggg aac ttc ttt tat tta ttt ttg tcg agc acc 971
 Val Leu Lys Phe Leu Gly Asn Phe Phe Tyr Leu Phe Leu Ser Ser Thr
 210 225
- tic ctt gga gta ttt gct gga ttg ctc agt gca tac ata atc aag aag 1019

 Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys Lys

 230 235 240
- cta tac att gga agg cat tct act gac cgt gag gtt gcc ctt atg atg 1067
 Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met
 245 250 255
- ctc alg gct lac cit ica tal alg ctg gct gag lig cla gat lig agc 1115 Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Leu Asp Leu Ser

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305

290

260 265 270

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ggc	att	ctc	acc	gta	t t c	ttc:	tgt	ggt	att	gta	atg	tca	cat	tac	act Thr	1163
Gly	Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	116	V a. i	Met	261	1113	1 7 1		
	275		٠			280					285					
tgg	cat	aac	gtc	aca	gag	agt	tca	aga	gtt	aca	aca	aag	cac	gca	ttt	1211
Trp	His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Val	Thr	Thr	Lys	His	Ala	Phe	

gca act ctg tcc ttc att gct gag act ttt ctc ttc ctg tat gtl ggg 1259
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310 315 320

300

- atg gat gca ttg gat att gaa aaa tgg gag ttt gcc agt gac aga cct 1307
 Met Asp Ala Leu Asp lle Glu Lys Trp Glu Phe Ala Ser Asp Arg Pro
 325 330 335
- ggc aaa tcc att ggg ata agc tca att ttg cta gga ttg gtt ctg att 1355 Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly Leu Val Leu Ile 340 345 350
- gga aga gct gct ttt gta ttc ccg ctg tcg ttc ttg tcg aac cta aca 1403 Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Thr 355 360 365

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Lys Lys Ala Pro Asn Glu Lys Ile Thr Trp Arg Gln Gln Val Val Ile	
200 385	
370 375	
tgg tgg gct ggg ctg atg aga gga gct gtg tcg att gct cti gct tac	1499
tgg tgg gct ggg ctg atg aga gg or or or or the Ala Leu Ala Tyr	
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390 395 400	
ant cat cag ctg cac ggc aat gca ata	1547
aat aag tit aca aga tot ggo cat act cag otg cac ggo aat goa ata	
Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala Ile	
405 410 415	
and at a star of a tit	1595
atg atc acc agc acc atc act gtc gtt ctt ttt agc act atg gta ttt	
Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val Phe	
430	
420	
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ggg atg atg aca aag cca ttg atc agg ctg ctg cta ccg gcc tca ggc	1010
Gly Met Met Thr Lys Pro Leu Ile Arg Leu Leu Pro Ala Ser Gly	
4.4.5	
435 440 445	
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His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser Pro	
4 h h	
450 455 460	

ctc ctg aca agc atg caa ggt tct gac ctc gag agt aca acc aac att 1739 Leu Leu Thr Ser Met Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn Ile 470 475 480

gig agg cct tcc agc ctc cgg atg ctc ctc acc aag ccg acc cac act 1787

Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His Thr

485

490

495

gtc cac tac tac tgg cgc aag ttc gac gac gcg ctg atg cga ccg atg 1835

Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Mct Arg Pro Mct

500 505 510

tti ggc ggg cgc ggg tic gig ccc tic tcc cci gga tca cca acc gag 1883

Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr Glu

515 520 525

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<213> Oryza sativa

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35 40 45

Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val
50 55 60

lle Leu Leu Met Thr Lys Gly Lys Ser Ser His Leu Phe Val Phe Ser

65 70 75 80

Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala 85 90 95

Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile
100 105 110

Thr Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser 115

lle Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly Thr Leu Asp 130 135 140

Val Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser 145

Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Phe Leu Tyr 165 170 175

Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Ile Val

Leu Phe Asn Ala Leu Gln Asn Phe Asp Leu Val His Ile Asp Ala Ala

Val Val Leu Lys Phe Leu Gly Asn Phe Phe Tyr Leu Phe Leu Ser Ser 210 215 220

Thr Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys
225 230 235 240

Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met
245 250 255

Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Leu Asp Leu
260 265 270

Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Mct Ser His Tyr 275 280 285

Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Ala
290 295 300

Phe Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val 305 310 310 315 315

Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Glu Phe Ala Ser Asp Arg

Pro Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly Leu Val Leu
340 345 350

lle Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu 355 360

Thr Lys Lys Ala Pro Asn Glu Lys Ile Thr Trp Arg Gln Gln Val Val
370 380

Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala 385 390 395 400

Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala
405 410 415

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420 425 430

Phe Gly Met Met Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser 435 440 445

Gly His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser 450

Pro Leu Leu Thr Ser Mei Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn 465 470 475 480

lle Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His

490

495

Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro 500 505 510

Met Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr 515

Glu Gln Ser His Gly Gly Arg 530 535